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Nucleotide

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1: G29810. human STS SHGC-35...[gi:1593361]

Links

LOCUS G29810 200 bp DNA linear STS 05-OCT-1996
DEFINITION human STS SHGC-35430, sequence tagged site.
ACCESSION G29810
VERSION G29810.1 GI:1593361
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 200)
AUTHORS Myers,R.M.
JOURNAL Unpublished (1996)
COMMENT

Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu

Primer A: AACCCATGTTCTCTGGGTGG
Primer B: CGGTGAGAGTAGAAACCACTAGG
STS size: 200
PCR Profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9600

Protocol:

Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Taq Polymerase: 0.05 units/ul
Total Vol: 10 ul

Buffer:

MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from Z48475
— Washington University/Merck EST sequence.

FEATURES
source Location/Qualifiers
1..200
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="2"
STS
1..200

primer bind 1..19
primer bind complement(178..200)
BASE COUNT 41 a 59 c 58 g 42 t
ORIGIN
1 aacccatgtt tctgggtggg tgaaaggggc ccaacctgc ccacttcagc ccagcccgcc
61 caaggggact tgtgccagca gaacatgtgg gaggaagaag ccccgtttc agggcatccg
121 cagcccaggy tagggagaaa tattctctcc actttggggg agagttcttg ctctcgacct
181 agtggtttct actctcacg
//

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UniSTS

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SHGC-35430

UniSTS:2990

Primer Information

Forward primer: AACCCATGTTTCTGGGTGG
Reverse primer: CGGTGAGAGTAGAAACCACTAGG
PCR product size: 200 (bp), Homo sapiens
GenBank Accession: G26769 G29810 Z48475

Homo sapiens

Name: SHGC-35430

Also known as: G26769, G29810, Z48475, SGC35430, RH37730,
RH56696, RH73632, STS_Z48475

Cross References

LocusLink LocusID: 2646
Symbol: GCKR
Description: glucokinase (hexokinase 4) regulatory protein
Position: 2p23
UniGene Hs.89771 glucokinase (hexokinase 4) regulatory protein
SNP rs704790 Summary
RH details RH37730 Genebridge4
RH37730 Stanford G3
RH56696 Genebridge4
RH73632 Genebridge4
RH73632 Stanford TNG

Mapping Information

View all results using the Map Viewer

SHGC-35430	Sequence Map:	Chr 2	mv
	Position:	27704016-27704215 (bp)	
SHGC-35430	SHGC-G3 Map:	Chr 2	mv
	Position:	1216 (cR10000)	
	Lod score:	F	
	Reference Interval:	1000:1 bin 9	
SHGC-35430	TNG Map:	Chr 2	mv
	Lod score:	8.1	
	Reference Interval:	61	
SGC35430	WI-RH Map:	Chr 2	mv

Position: 146.6 (cR3000)
Lod score: P0.68

SHGC-35430 GM99-G3 Map: Chr 2 mv
Position: 1211 (cR10000)
Lod score: F
Reference Interval: D2S171-D2S165 (48.5-50.7 cM)

SGC35430 GM99-GB4 Map: Chr 2 mv
Position: 97.79 (cR3000)
Lod score: 0.01
Reference Interval: D2S165-D2S352 (50.7-54.1 cM)

Electronic PCR results

RefSeq mRNA (1)

NM_001486.1 1944 .. 2143 Homo sapiens glucokinase
(hexokinase 4) regulatory protein
(GCKR) mRNA (2197 bp)

mRNA (1)

Z48475.1 1941 .. 2140 H.sapiens GCKR mRNA for
glucokinase regulator (2194 bp)

Working Draft phase 1 (from GenBank HTGS division) (1)

AC009427.2 106322 .. 106521 Homo sapiens clone RP11-45M3,
WORKING DRAFT SEQUENCE,
25 unordered pieces (163455 bp)

ESTs (5 of 7)[Show All Hits]

AV718702.1	33 .. 232	AV718702 GLC Homo sapiens cDNA clone GLCGHE03 5'' (589 bp)
W86849.1	46 .. 245	zh59d01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416353 3'' (435 bp)
C20978.1	25 .. 224	HUMGS0002450 Human adult (K.Okubo) Homo sapiens cDNA 3' (275 bp)
AA700791.1	44 .. 242	zi66c06.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435754 3'' similar to SW:GCKR_HUMAN Q14397 GLUCOKINASE REGULATORY PROTEIN ; (497 bp)
AI125712.1	46 .. 245	qd95c02.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1737218 3'' similar to SW:GCKR_HUMAN Q14397 GLUCOKINASE REGULATORY PROTEIN ; (806 bp)

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1: G22557. human STS WI-1108...[gi:1342883]

Links

LOCUS G22557 337 bp DNA linear STS 31-MAY-1996
DEFINITION human STS WI-11083, sequence tagged site.
ACCESSION G22557
VERSION G22557.1 GI:1342883
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 337)

AUTHORS Hudson,T.

TITLE Whitehead Institute/MIT Center for Genome Research; Physically
Mapped STSs

JOURNAL Unpublished (1995)

COMMENT

Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu

Primer A: TTTCATTTTATTTCACTTGGGATAGG

Primer B: CTTGGTTTFTGGGGGAATAT

STS size: 126

PCR Profile:

Presoak:

Denaturation:

Annealing: 56 degrees C

Polymerization:

PCR Cycles: 35

Thermal Cycler:

Protocol:

Template: 10 ng

Primer: each 5 pM

dNTPs: each 4 nM

Taq Polymerase: 0.025 units/ul

Total Vol: 20 ul

Buffer:

MgCl2: 1.5 mM

KCl: 50 mM

Tris-HCL: 10 mM

pH: 9.3

Derived from dbEST (genbank accession R39575).

FEATURES

source

Location/Qualifiers

1..337

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/map="529.6 cR from top of Chr2 linkage group"

STS

13..138

primer bind 13..37
primer bind complement(119..138)
BASE COUNT 89 a 70 c 80 g 96 t 2 others
ORIGIN
1 tgaattattt catttcattt atttcacttg ggataggatt gaaagtcttg atgatgaggc
61 catagcacag tcagaccatc tgcttttcca gttctgtgtt tgcaccgtct gtgcatccat
121 attcccccca aaaccaagaa ggccagtga aagtggggcca gcacaatgcc ccagggngga
181 acgtgggagg aggtctcctt gactgtgggt gcgtaggtgt ctgaaaactc aggttattat
241 gggacaacac atttaaaatc catgtgcaaa tcctctcttg tgacagggat caaaaatcaa
301 tgggcacttc aatgtaggtc tcattatttt ctgnata

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UniSTS

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UniSTS:81693

Primer Information

Forward primer: **TTTCATTTATTTCACCTGGGATAGG**
Reverse primer: **CTTGGTTTTGGGGGAATAT**
PCR product size: 126 (bp), Homo sapiens
GenBank Accession: G22557 R39575

Homo sapiens

Name: WI-11083
Also known as: G22557, R39575, RH57066, EST209637

Cross References

UniGene	Hs.25333	interleukin 1 receptor, type II
SNP	rs3218953	Summary
RH details	RH57066	Genebridge4

Mapping Information**View all results using the Map Viewer**

WI-11083	Sequence Map:	Chr 2	mv
	Position:	102249311-102249436 (bp)	
WI-11083	WI-RH Map:	Chr 2	mv
	Position:	522.6 (cR3000)	
	Lod score:	P2.31	
WI-11083	GM99-GB4 Map:	Chr 2	mv
	Position:	357.75 (cR3000)	
	Lod score:	3.00	
	Reference Interval:	D2S113-D2S176 (115.3-120.8 cM)	

Electronic PCR results**ESTs (1)**

R39575.1 13 .. 138 yh96d04.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:137575 3' similar to gb:X59770 INTERLEUKIN-1 RECEPTOR, TYPE II PRECURSOR (HUMAN); (337 bp)

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SHGC-35324

UniSTS:48271

Primer Information

Forward primer:

GCCAAGAGTTCTTTAGGTGCC

Reverse primer:

TTTTTAAAGATCTTCCAAGCC

PCR product size:

205 (bp), Homo sapiens

GenBank Accession:

G26702 G28576 M27492

Homo sapiens

Name: SHGC-35324

Also known as: G26702, G28576, M27492, SGC35324, RH37701, RH57058, RH71645, STS_M27492

Cross References

LocusLink	LocusID:	3554
	Symbol:	IL1R1
	Description:	interleukin 1 receptor, type I
	Position:	2q12
UniGene	Hs:82112	interleukin 1 receptor, type I
RH details	RH37701	Genebridge4
	RH37701	Stanford G3
	RH57058	Genebridge4
	RH71645	Genebridge4
	RH71645	Stanford TNG

Mapping Information

View all results using the Map Viewer

SHGC-35324	Sequence Map:	Chr 2	mv
	Position:	102397803-102398007 (bp)	
SGC35324	WI-RH Map:	Chr 2	mv
	Position:	521.7 (cR3000)	
	Lod score:	P>3.00	
SHGC-35324	TNG Map:	Chr 2	mv
	Lod score:	15.7	
	Reference Interval:	181	
SHGC-35324	GM99-G3 Map:	Chr 2	mv
	Position:	5327 (cR10000)	
	Lod score:	1.82	

SGC35324 GM99-GB4 Map: Chr 2 mv
Position: 356.67 (cR3000)
Lod score: 3.00
Reference Interval: D2S113-D2S176 (115.3-120.8 cM)

RefSeq mRNA (1)

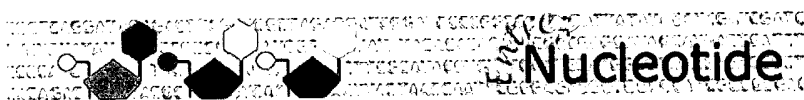
mRNA (1)

Genomic (1)

Working Draft phase 1 (from GenBank HTGS division) (2)

AC139506.1 158866 .. 159070 Homo sapiens chromosome 5 clone
RP11-911K5, WORKING
DRAFT SEQUENCE, 43
unordered pieces (289192 bp)

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Limits

Display Show:

1: G14572. human STS SHGC-11...[gi:1130311]

Links

LOCUS G14572 347 bp DNA linear STS 04-JAN-1996
 DEFINITION human STS SHGC-11498, sequence tagged site.
 ACCESSION G14572
 VERSION G14572.1 GI:1130311
 KEYWORDS STS; STS sequence; primer; sequence tagged site.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 347)
 AUTHORS Myers,R.M.
 JOURNAL Unpublished (1995)
 COMMENT

Contact: Richard M. Myers
 Stanford Human Genome Center (SHGC)
 Stanford University School of Medicine
 Department of Genetics, M-344, Stanford, CA 94305, USA
 Tel: 4157259687
 Fax: 4157259689
 Email: myers@shgc.stanford.edu

Primer A: GAATTAAATGAGGGCTGAAACG

Primer B: CATGTGCATATTTTCATCCCG

STS size: 131

PCR Profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds

Annealing: 62 degrees C for 23 seconds

Polymerization: 72 degrees C for 30 seconds

PCR Cycles: 30

Thermal Cycler: Perkin Elmer 9600

Protocol:

Template: 25 ng

Primer: each 1 uM

dNTPs: each 200 uM

Taq Polymerase: 0.05 units/ul

Total Vol: 10 ul

Buffer:

MgCl2: 2.5 mM

KCl: 50 mM

Tris-HCl: 20 mM

pH: 8.3

Prepared with primer pairs derived from T52830--Merck/UniEST.

FEATURES

source

Location/Qualifiers

1..347

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/map="2"

STS

116..246

primer bind

116..137

primer bind complement(226..246)
BASE COUNT 97 a 67 c 65 g 99 t 19 others
ORIGIN
1 ttttagnttt tttagccna tatatgacta tanggagtc ngtagataaa tacgagccca
61 cnnnnnnnnn ncagcctanc ctccccaca gaggtgctg cgctacttac aaattgaatt
121 aaatgagggc tgaacggca cgcttcagca tgtactgtag tcacogtga agaacaagtc
181 ttccaatat tggggcatgt attgatttct aaaaaatgtc tgectgggga atgaaatatg
241 cacatgtatt tcatattcac agatctgctt ccgaaaacct ctctatttaa tatcactcaa
301 ttatgaaatt tggttttgct ttcagaggga anggaatngc attncag

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H. sapiens

M. musculus

R. norvegicus

D. rerio

SHGC-11498

UniSTS:42735

Primer Information

Forward primer:

GAATTAAATGAGGGCTGAAACG

Reverse primer:

CATGTGCATATTTTCATTCCCC

PCR product size:

131 (bp), Homo sapiens

GenBank Accession:

G14572 T52830

Homo sapiens

Name: SHGC-11498

Also known as: G14572, T52830, RH13879, D2S2836, gdb:733324, gdb:735490

Cross References

LocusLink LocusID: 3488

Symbol: IGFBP5

Description: insulin-like growth factor binding protein 5

Position: 2q33-q36

UniGene Hs.380833 insulin-like growth factor binding protein 5

RH details RH13879 Genebridge4

RH13879 Stanford G3

GDB D2S2836
gdb:733324
gdb:735490

Mapping Information

View all results using the Map Viewer

SHGC-11498 Sequence Map: Chr 2 mv
Position: 217504614-217504744 (bp)SHGC-11498 NCBI RH Map: Chr 2 mv
Position: 1652.7 (cR)
Lod score: 1.62SHGC-11498 SHGC-G3 Map: Chr 2 mv
Position: 8508 (cR10000)
Lod score: F
Reference Interval: 1000:1 bin 116SHGC-11498 GM99-G3 Map: Chr 2 mv
Position: 9347 (cR10000)

Lod score: F

Reference Interval: D2S164-D2S163 (222.0-225.6 cM)

Electronic PCR results**mRNA (2)**

L27560.1 2 .. 132 Human insulin-like growth factor binding protein 5 (IGFBP5) mRNA (3672 bp)
AF147308.1 124 .. 254 Homo sapiens full length insert cDNA clone YA81B05 (374 bp)

Genomic (2)

L27559.1 1124 .. 1254 Human insulin-like growth factor binding protein 5 (IGFBP5) gene, partial exon 4 (1303 bp)
AH003147.1 3565 .. 3695 Human insulin-like growth factor binding protein 5 (IGFBP5) gene (3744 bp)

ESTs (5 of 18)[Show All Hits]

AV746775.1 158 .. 288 AV746775 NPC Homo sapiens cDNA clone NPCBJE02 5' (389 bp)
AU140606.1 518 .. 649 AU140606 PLACE3 Homo sapiens cDNA clone PLACE3000376 5' (776 bp)
AU140627.1 442 .. 572 AU140627 PLACE3 Homo sapiens cDNA clone PLACE3000412 5' (776 bp)
AU140641.1 67 .. 197 AU140641 PLACE3 Homo sapiens cDNA clone PLACE3000434 5' (812 bp)
BF923964.1 63 .. 193 MR2-NT0138-301100-004-g07 NT0138 Homo sapiens cDNA (521 bp)

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MGD

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Resources

H. sapiens

M. musculus

R. norvegicus

D. rerio

D6S1941

UniSTS:20217

Primer Information

Forward primer:

ATGTGATTATGTGGTACCTTGGC

Reverse primer:

AATCGTATACAACATTTCACATGGC

PCR product size:

335-336 (bp), Homo sapiens

GenBank Accession:

G06545 X80910

Homo sapiens

Name: D6S1941

Also known as: , G06545, X80910, WI-7372, UTR-05277, G00-679-154

Cross References

LocusLink LocusID: 5500

Symbol: PPP1CB

Description: protein phosphatase 1, catalytic subunit, beta isoform

Position: 2p23

UniGene Hs.21537 protein phosphatase 1, catalytic subunit, beta isoform

SNP rs15462 Summary

GDB GDB:679154

G00-679-154

Mapping Information

View all results using the Map Viewer

D6S1941	Sequence Map:	Chr 2	mv
	Position:	28980687-28981022 (bp)	

Electronic PCR results

RefSeq mRNA (1)

NM_002709.1 2050 .. 2385 Homo sapiens protein phosphatase 1, catalytic subunit, beta isoform (PPP1CB) mRNA (3590 bp)

mRNA (3)

BC002697.1 1882 .. 2216 Homo sapiens, protein phosphatase 1, catalytic subunit, beta isoform, clone MGC:3672, mRNA, complete cds (2875)

bp)
BC012045.1 1873 .. 2207 Homo sapiens, Similar to protein
phosphatase 1, catalytic subunit, beta
isoform, clone MGC:10563
IMAGE:3631338, mRNA, complete cds
(2872 bp)
X80910.1 2050 .. 2385 H.sapiens PPP1CB mRNA (3590 bp)

ESTs (2)

AU141166.1 268 .. 603 AU141166 THYRO1 Homo sapiens
cDNA clone THYRO1000120 5' (729
bp)
BG925280.1 189 .. 522 HNC71-1-D3.R HNC (Human Normal
Cartilage) Homo sapiens cDNA (577
bp)

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UniSTS

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D10S2186

UniSTS:72899

Primer Information

Forward primer: TGGACATTTTCATACCTGTGCA
Reverse primer: ACCTACCCTGAGGTCCGTCT
PCR product size: 113-114 (bp), Homo sapiens
GenBank Accession: G07262 U15932

Homo sapiens

Name: D10S2186
Also known as: , G07262, U15932, WI-9369, RH51344, UTR-05734,
G00-678-253

Cross References

LocusLink	LocusID:	1847
	Symbol:	DUSP5
	Description:	dual specificity phosphatase 5
	Position:	10q25
UniGene	Hs.2128	dual specificity phosphatase 5
RH details	RH51344	Genebridge4
GDB	GDB:678253	
	G00-678-253	

Mapping Information**View all results using the Map Viewer**

D10S2186 Sequence Map:	Chr 10	mv
Position:	112401473-112401586 (bp)	
WI-9369 NCBI RH Map:	Chr 10	mv
Position:	1179 (cR)	
Lod score:	1.17	
WI-9369 WI-YAC Map:	Chr 10	mv
Position:	423 (ordinal)	
Reference Interval:	WC10.10	
WI-9369 WI-RH Map:	Chr 10	mv
Position:	604.1 (cR3000)	
Lod score:	P0.00	
WI-9369 GM99-GB4 Map:	Chr 10	mv

Position: 506.37 (cR3000)
Lod score: 0.80
Reference Interval: D10S597-D10S1681 (137.6-141.8 cM)

Electronic PCR results

RefSeq mRNA (1)

NM_004419.2 1428 .. 1541 Homo sapiens dual specificity
phosphatase 5 (DUSP5), mRNA (2473
bp)

mRNA (1)

U15932.2 1425 .. 1538 Human dual-specificity protein
phosphatase mRNA, complete cds (2470
bp)

ESTs (5 of 9)[Show All Hits]

BE790490.1	251 .. 366	601480662F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3883526 5' (933 bp)
BG337015.1	222 .. 335	602434472F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4552577 's; (948 bp)
BF175321.1	62 .. 175	MYE4874 Myeloma (MYE) cDNA library Homo sapiens cDNA (295 bp)
BG773878.1	692 .. 805	602661578F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4810123 5' (876 bp)
BI088593.1	23 .. 136	602853138F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:4994816 5' (772 bp)

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1: G14649. human STS SHGC-11...[gi:1130388]

Links

LOCUS G14649 400 bp DNA linear STS 04-JAN-1996
DEFINITION human STS SHGC-11749, sequence tagged site.
ACCESSION G14649
VERSION G14649.1 GI:1130388
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 400)
AUTHORS Myers,R.M.
JOURNAL Unpublished (1995)
COMMENT

Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu

Primer A: TTTCCTTTTATTGGAAAAGTCAGC

Primer B: TGCTAACCCCGTCGCTC

STS size: 240

PCR Profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds

Annealing: 64 degrees C for 23 seconds

Polymerization: 72 degrees C for 30 seconds

PCR Cycles: 30

Thermal Cycler: Perkin Elmer 9600

Protocol:

Template: 25 ng

Primer: each 1 uM

dNTPs: each 200 uM

Taq Polymerase: 0.05 units/ul

Total Vol: 10 ul

Buffer:

MgCl₂: 2.5 mM

KCl: 50 mM

Tris-HCl: 20 mM

pH: 8.3

Prepared with primer pairs derived from T59429—Merck/UniEST.

FEATURES
source 1..400
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="22"
STS 10..249
primer_bind 10..33

primer bind complement(232..249)
BASE COUNT 98 a 96 c 126 g 77 t 3 others
ORIGIN
1 gaggagtgnt ttcctttatt tggaaaagtc agcaacatgg atatggttca gaaaaaaaca
61 cagaaggagc aaaactaaca tgaacataga aagggggcct ttgataaaac gtcgaacaca
121 tcactattct gaggaaggag aggtttgcgt tgtttctagt aagacacagc cctctgtggc
181 accaaggggc tctcatgtcc agtccagggc ccagtcctct gcgggagggg ggagcagacg
241 gggtagcac ccgttaatct cgaggggtct tgagtgcagc ccagcgcccc tgcgaggtag
301 tctctgaggg tcgggggtca gtgctgggtc agcagcggcc atcccggggg ctttaggggn
361 ccaaggntcc aggggocggt caccagcag ggaccctca

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MIM *142600

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LocusLink

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***142600**

Links

HEXOKINASE 1; HK1Gene map locus [10q22](#)**TEXT****DESCRIPTION**

Hexokinase (EC 2.7.1.1) catalyzes the first step in glucose metabolism, utilizing ATP for the phosphorylation of glucose to glucose-6-phosphate. HK1 is normally cytoplasmic or associated with the outer mitochondrial membrane via an interaction with porin (VDAC1; [604492](#)), a voltage-dependent anion channel.

CLONING

[Nishi et al. \(1988\)](#) analyzed cDNA clones encoding human hexokinase isolated from an adult kidney library. Analysis of this 917-amino acid protein showed that the sequences of the N- and C-terminal halves, corresponding to the regulatory and catalytic domains, respectively, are homologous. Eukaryotic hexokinases evolved from duplication of a gene encoding a protein of about 450 amino acids. [Griffin et al. \(1991\)](#) thought that comparisons of sequences in many species supported the theory of [Ureta \(1982\)](#) that the mammalian hexokinases arose from the duplication and fusion of an ancestral protoenzyme and that the yeast and mammalian glucokinases arose twice in evolution. In the course of their work, [Griffin et al. \(1991\)](#) developed a method for cloning the cDNA for a low abundance protein using knowledge of the evolutionary conservation of amino acid and nucleotide sequence.

Spermatogenic cell-specific hexokinase ([142550](#)) was found by [Mori et al. \(1993\)](#) to contain unique sequences at the 5-prime terminus which lacks a porin-binding domain (PBD). The PBD of HK1 comprises a 15-amino acid sequence that is absolutely conserved and mediates its binding to the mitochondria.

[Murakami and Piomelli \(1997\)](#) identified the cDNA for human red blood cell-specific hexokinase. They found that its nucleotide sequence was identical to that previously identified for HK1 cDNA except for the extreme 5-prime end. It lacks the first 62 nucleotides of the HK1 coding region; instead, it contains a unique sequence of 60 nucleotides at the beginning of the coding sequence as well as another unique sequence upstream of the putative translation initiation site. It lacks the porin-binding domain that facilitates binding to mitochondria, thus explaining the exclusive cytoplasmic localization of red blood cell HK. It was the major cDNA derived from reticulocytes, consistent with the observation that the activity of this isoform of the enzyme is predominant in reticulocytes. Northern blot analysis showed that it was expressed in reticulocytes and in an erythroleukemic cell line, but not in a lymphocytic cell line.

GENE STRUCTURE

[Ruzzo et al. \(1998\)](#) determined that the HK1 gene contains 18 exons and spans about 75 kb.



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Genome

Resources

[H. sapiens](#)[M. musculus](#)[R. norvegicus](#)[D. rerio](#)**WI-9162**

UniSTS:78319

Primer Information

Forward primer: **TTCCATTATTTCTTTGATCTTCAGG**
Reverse primer: **GCTGGGTGTGGACAGGAC**
PCR product size: **113-114 (bp), Homo sapiens**
GenBank Accession: **G07156 J03600**

Homo sapiens

Name: **WI-9162**
Also known as: **G07156, J03600, ALOX5, UTR-02604, G00-678-148**

Cross References

LocusLink	LocusID:	240
	Symbol:	ALOX5
	Description:	arachidonate 5-lipoxygenase
	Position:	10q11.2
UniGene	Hs.89499	arachidonate 5-lipoxygenase
GDB	GDB:678148	
	G00-678-148	

Mapping Information**View all results using the Map Viewer**

WI-9162	Sequence Map:	Chr 10	mv
	Position:	45716454-45716565 (bp)	

Electronic PCR results**RefSeq mRNA (1)**

NM_000698.1 2192 .. 2305 Homo sapiens arachidonate 5-lipoxygenase (ALOX5) mRNA (2497 bp)

mRNA (2)

J03600.1 2192 .. 2305 Human lipoxygenase mRNA, complete cds (2497 bp)

J03571.1 2181 .. 2292 Human 5-lipoxygenase mRNA, complete cds (2484 bp)

ESTs (5 of 24)[Show All Hits]

BI712395.1	366 .. 477	ie07c05.x1 HR85 islet Homo sapiens cDNA 3' similar to SW:LOX5_HUMAN P09917 ARACHIDONATE 5-LIPOXYGENASE ; (602 bp)
BI712628.1	220 .. 331	ie07c05.y1 HR85 islet Homo sapiens cDNA 5' similar to SW:LOX5_HUMAN P09917 ARACHIDONATE 5-LIPOXYGENASE ; (625 bp)
AA552112.1	125 .. 236	nk05f07.s1 NCI_CGAP_Co2 Homo sapiens cDNA clone IMAGE:1012645 3' similar to gb:J03600 ARACHIDONATE 5-LIPOXYGENASE (HUMAN); (499 bp)
AA552491.1	124 .. 235	nk12e11.s1 NCI_CGAP_Co2 Homo sapiens cDNA clone IMAGE:1013324 3' similar to gb:J03600 ARACHIDONATE 5-LIPOXYGENASE (HUMAN); (501 bp)
AA593920.1	192 .. 303	nn20e03.s1 NCI_CGAP_Co12 Homo sapiens cDNA clone IMAGE:1084444 3' similar to gb:J03600 ARACHIDONATE 5-LIPOXYGENASE (HUMAN); (541 bp)

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UniSTS

Search for **SHGC-30316**

UniSTS:35867

Primer Information

Forward primer: **CTAGAAGACAGCAGTGACACTTCC**
Reverse primer: **TGGGGTAGTTTGGCTGCC**
PCR product size: 150 (bp), Homo sapiens
GenBank Accession: G27080 R45056

Homo sapiens

Name: SHGC-30316
Also known as: G27080, R45056, RH14850

Cross References

LocusLink	LocusID:	84990
	Symbol:	MGC14433
	Description:	hypothetical protein MGC14433
	Position:	12q24.21
UniGene	Hs.83572	hypothetical protein MGC14433
RH details	RH14850	Genebridge4
	RH14850	Stanford G3

Mapping Information**View all results using the Map Viewer**

SHGC-30316	Sequence Map:	Chr 12	mv
	Position:	112728430-112728579 (bp)	
SHGC-30316	NCBI RH Map:	Chr 12	mv
	Position:	720.1 (cR)	
	Lod score:	2.55	
SHGC-30316	SHGC-G3 Map:	Chr 12	mv
	Position:	4759 (cR10000)	
	Lod score:	F	
	Reference Interval:	1000:1 bin 89	
SHGC-30316	GM99-G3 Map:	Chr 12	mv
	Position:	4705 (cR10000)	
	Lod score:	F	
	Reference Interval:	D12S78-D12S79 (113.3-126.1 cM)	

Electronic PCR results**ESTs (5 of 6)[Show All Hits]**

BF948718.1 203 .. 352 CM2-NN1152-311000-454-c05 NN1152
Homo sapiens cDNA (392 bp)
BM015957.1 394 .. 543 603642364F1 NIH_MGC_87 Homo
sapiens cDNA clone IMAGE:5418495
' (820 bp)
AA336813.1 7 .. 156 EST41539 Endometrial tumor Homo sapiens
cDNA 5' end (299 bp)
AI161072.1 198 .. 344 qc77g11.x1
Soares_placenta_8to9weeks_2NbHP8to9W
Homo sapiens cDNA clone
IMAGE:1715684 3' (406 bp)
AW955941.1 6 .. 155 EST368011 MAGE resequences, MAGD
Homo sapiens cDNA (460 bp)

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D12S1892

UniSTS:51878

Primer Information

Forward primer: **GGAGAGGACTGGGAAGGGATC**
Reverse primer: **TGCCAAAATTCTAGAGGATAAAGG**
PCR product size: 145 (bp), Homo sapiens
GenBank Accession: G11327 M32402

Homo sapiens

Name: D12S1892
Also known as: , G11327, M32402, RH2069, SHGC-9798, gdb:675595

Cross References

LocusLink	LocusID:	8909
	Symbol:	P11
	Description:	26 serine protease
	Position:	12q13.1
UniGene	Hs.997	protease, serine, 22
RH details	RH2069	Genebridge4
	RH2069	Stanford G3
GDB	GDB:674927	
	gdb:675595	

Mapping Information**View all results using the Map Viewer**

D12S1892	Sequence Map:	Chr 12	mv
	Position:	47821110-47821254 (bp)	
SHGC-9798	NCBI RH Map:	Chr 12	mv
	Position:	382.3 (cR)	
	Lod score:	1.93	
SHGC-9798	SHGC-G3 Map:	Chr 12	mv
	Position:	1891 (cR10000)	
	Lod score:	F	
	Reference Interval:	1000:1 bin 32	
SHGC-9798	GM99-G3 Map:	Chr 12	mv
	Position:	1837 (cR10000)	
	Lod score:	F	

Reference Interval: D12S333-D12S325 (53.3-70.6 cM)

Electronic PCR results

RefSeq mRNA (1)

NM_006025.2 1342 .. 1486 Homo sapiens protease, serine, 22 (P11), mRNA (2321 bp)

mRNA (3)

M32402.1 1342 .. 1486 Human placental protein (PP11) mRNA, complete cds (2320 bp)
M36109.1 1342 .. 1486 Human placental protein 11 (PP11) mRNA (2320 bp)
AK075446.1 1434 .. 1578 Homo sapiens cDNA PSEC0138 fis, clone PLACE1005659, highly similar to Human placental protein (PP11) mRNA (2413 bp)

Working Draft phase 1 (from GenBank HTGS division) (1)

AP001134.2 92985 .. 93129 Homo sapiens chromosome 18 clone RP11-785E17 map 18q12, WORKING DRAFT SEQUENCE, in unordered pieces (158412 bp)

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H. sapiens

M. musculus

R. norvegicus

D. rerio

D12S2023

UniSTS:7967

Primer Information

Forward primer:

ACAGGAGGATTAAACAGACAGAGG

Reverse primer:

TTATTTAATTGTGTTTTAGAGGGCA

PCR product size:

308-309 (bp), Homo sapiens

GenBank Accession:

G06363 M11568

Homo sapiens**Name:** D12S2023**Also known as:** , G06363, M11568, WI-7033, UTR-02138, G00-678-964**Cross References****LocusLink** LocusID: 3479

Symbol: IGF1

Description: insulin-like growth factor 1 (somatomedin C)

Position: 12q22-q23

UniGene Hs.85112 insulin-like growth factor 1 (somatomedin C)**GDB** GDB:678964
G00-678-964**Mapping Information****View all results using the Map Viewer**

WI-7033

WI-YAC Map:

Chr 12

mv

Position:

386 (ordinal)

Reference Interval:

WC12.5

Electronic PCR results**mRNA (1)**M11568.1 774 .. 1082 Human insulin-like growth factor IB (IGF-IB)
cDNA to mRNA (1094 bp)**Questions or Comments?**
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UniSTS

Search UniSTS ☐ for Go**D12S1970**

UniSTS:72432

Primer Information

Forward primer: **TGCTGCATAAATCACTTATCGG**
Reverse primer: **GAACACAAATTTCTGAAAGGTGC**
PCR product size: 105-106 (bp), Homo sapiens
GenBank Accession: G07226 U02680

Homo sapiens

Name: D12S1970
Also known as: , G07226, U02680, WI-9296, UTR-04614,
G00-678-220

Cross References

LocusLink	LocusID:	5756
	Symbol:	PTK9
	Description:	PTK9 protein tyrosine kinase 9
	Position:	12q12
UniGene	Hs.82643	PTK9 protein tyrosine kinase 9
GDB	GDB:678220	
	G00-678-220	

Mapping Information

D12S1970	Sequence Map:	Chr 12	mv
	Position:	43904891-43904996 (bp)	
D12S1970	Sequence Map:	Chr 17	mv
	Position:	27381065-27381170 (bp)	
WI-9296	WI-YAC Map:	Chr 12	mv
	Position:	151 (ordinal)	
	Reference Interval:	WC12.1	

Electronic PCR results**RefSeq mRNA (2)**

XM_208162.1 2253 .. 2358	Homo sapiens similar to protein tyrosine kinase 9 [Homo sapiens] (LOC284087), mRNA (2991 bp)
NM_002822.1 2251 .. 2356	Homo sapiens protein tyrosine kinase 9 (PTK9) mRNA (3000 bp)

mRNA (3)

BC022344.1	2289 .. 2394	Homo sapiens, protein tyrosine kinase 9, clone MGC:23788 IMAGE:4249251, mRNA, complete cds (3040 bp)
BC043148.1	2325 .. 2430	Homo sapiens, PTK9 protein tyrosine kinase 9, clone MGC:41876 IMAGE:5297068, mRNA, complete cds (3085 bp)
U02680.1	2251 .. 2356	Human protein tyrosine kinase mRNA, complete cds (3000 bp)

Working Draft phase 1 (from GenBank HTGS division) (3)

AC126390.8	146458 .. 146563	Homo sapiens chromosome 15 clone CTD-2505124 map 15, *** SEQUENCING IN PROGRESS *** , 3 unordered pieces (189762 bp)
AC021719.3	59292 .. 59397	Homo sapiens chromosome 4 clone RP11-210N13 map 4, WORKING DRAFT SEQUENCE, 14 unordered pieces (165868 bp)
AC027810.3	21708 .. 21813	Homo sapiens chromosome 18 clone RP11-357J12 map 18, WORKING DRAFT SEQUENCE, 14 unordered pieces (155628 bp)

ESTs (5 of 20)[Show All Hits]

BE865490.1	304 .. 409	601677821F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3960652 5' (638 bp)
AV730589.1	73 .. 178	AV730589 HTF Homo sapiens cDNA clone HTFAAC01 5' (721 bp)
AV732777.1	49 .. 154	AV732777 HTF Homo sapiens cDNA clone HTFANE11 5' (689 bp)
BF107297.1	92 .. 197	601824195F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4044095 5' (718 bp)
AU129391.1	227 .. 332	AU129391 NT2RP2 Homo sapiens cDNA clone NT2RP2005449 5' (848 bp)

Mus musculus

Name: D12S1970

Electronic PCR results**ESTs (1)**

AI526480.1	20 .. 124	pro646-8.E11.r prsdxcg Mus musculus cDNA 5' (681 bp)
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(13)



UniSTS

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D12S1945

UniSTS:28476

Primer Information

Forward primer: **CATGTGCTGCATGAAGAGCT**
Reverse primer: **AAGCTGCATAAATAGTAAGCAAAGG**
PCR product size: 349-350 (bp), Homo sapiens
GenBank Accession: G06781 S70004

Homo sapiens

Name: D12S1945
Also known as: G06781, S70004, WI-7963, WIAF-1343, RH52647,
UTR-05409, G00-677-760

Cross References

LocusLink	LocusID:	2998
	Symbol:	GYS2
	Description:	glycogen synthase 2 (liver)
	Position:	12p12.2
UniGene	Hs.82614	glycogen synthase 2 (liver)
SNP	rs936, rs984	Summary
RH details	RH52647	Genebridge4
GDB	GDB:677760	
	G00-677-760	

Mapping Information**View all results using the Map Viewer**

D12S1945	Sequence Map:	Chr 12	mv
	Position:	21589799-21590148 (bp)	
WI-7963	NCBI RH Map:	Chr 12	mv
	Position:	213.2 (cR)	
	Lod score:	1.79	
WI-7963	WI-YAC Map:	Chr 12	mv
	Position:	81 (ordinal)	
	Reference Interval:	WC12.1	
WI-7963	WI-RH Map:	Chr 12	mv
	Position:	158.7 (cR3000)	
	Lod score:	P1.70	

WIAF-1343 GM99-GB4 Map: Chr 12 mv
Position: 80.72 (cR3000)
Lod score: 0.00
Reference Interval: D12S358-D12S1596 (27.2-48.1 cM)

Electronic PCR results

mRNA (1)

S70004.1 2144 .. 2493 glycogen synthase [human, liver, mRNA,
2912 nt] (2912 bp)

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UniSTS

Search UniSTS for Go**SHGC-31640**

UniSTS:60918

Primer Information

Forward primer: **TAATCAAATTACCCACCCAAAGG**
Reverse primer: **GCCTTAGGCTGTGTGATAAACC**
PCR product size: **220 (bp), Homo sapiens**
GenBank Accession: **D64053 G27089**

Homo sapiens

Name: **SHGC-31640**
Also known as: **D64053, G27089, SGC31640, RH14859, RH52602, STS_D64053**

Cross References

LocusLink LocusID: **5801**
Symbol: **PTPRR**
Description: **protein tyrosine phosphatase, receptor type, R**
Position: **12q15**
UniGene Hs.198288 **protein tyrosine phosphatase, receptor type, R**
RH details RH14859 **Genebridge4**
RH14859 **Stanford G3**
RH52602 **Genebridge4**

Mapping Information**View all results using the Map Viewer**

SHGC-31640	Sequence Map:	Chr 12	mv
	Position:	70749450-70749669 (bp)	
SGC31640	WI-RH Map:	Chr 12	mv
	Position:	396.4 (cR3000)	
	Lod score:	P1.32	
SHGC-31640	GM99-G3 Map:	Chr 12	mv
	Position:	2839 (cR10000)	
	Lod score:	F	
	Reference Interval:	D12S83-D12S350 (76.5-87.6 cM)	
SGC31640	GM99-GB4 Map:	Chr 12	mv
	Position:	299.65 (cR3000)	
	Lod score:	0.82	
	Reference Interval:	D12S83-D12S350 (76.5-87.6 cM)	

Electronic PCR results**RefSeq mRNA (2)**

NM_002849.2 2432 .. 2651 Homo sapiens protein tyrosine phosphatase, receptor type, R (PTPRR), transcript variant 1, mRNA (3492 bp)

NM_130846.1 1673 .. 1892 Homo sapiens protein tyrosine phosphatase, receptor type, R (PTPRR), transcript variant 2, mRNA (2733 bp)

mRNA (5 of 6)[Show All Hits]

X82635.1 1653 .. 1872 H.sapiens mRNA for protein-tyrosine-phosphatase (2736 bp)

Z79693.1 2100 .. 2319 H.sapiens mRNA for protein-tyrosine phosphatase NC-PTPCOM1 (3033 bp)

U77917.1 1673 .. 1892 Human Ch-1PTPase gamma minus form mRNA, complete cds (2401 bp)

AK091647.1 669 .. 888 Homo sapiens cDNA FLJ34328 fis, clone FEBRA2009074, moderately similar to Human Ch-1PTPase delta form mRNA (1729 bp)

U42361.1 2190 .. 2409 Human protein tyrosine phosphatase Cr1PTPase precursor (Ch-1PTPase alpha) mRNA, complete cds (3250 bp)

Working Draft phase 1 (from GenBank HTGS division) (1)

AC015544.19 75099 .. 75318 Homo sapiens chromosome 12 clone RP11-1007B5, WORKING DRAFT SEQUENCE, 7 unordered pieces (206512 bp)

ESTs (1)

BG752351.1 297 .. 516 602730826F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4874430 5' (672 bp)

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D10S2285

UniSTS:17326

Primer Information

Forward primer: **ATAATTGCTTGTTTTCTAGCCTGG**
Reverse primer: **TAAATTGGAGTGGAAATAAAAACTGG**
PCR product size: 338-339 (bp), Homo sapiens
GenBank Accession: G06444 J05550

Homo sapiens

Name: D10S2285
Also , G06444, J05550, WI-7191, WIAF-1355, RH8302,
known as: UTR-02762, SHGC-12453, G00-679-049

Cross References

LocusLink LocusID: 4360
Symbol: MRC1
Description: mannose receptor, C type 1
Position: 10p13
UniGene Hs.75182 mannose receptor, C type 1
SNP rs506524, rs692520, rs692527, rs941, rs981 Summary
RH details RH8302 Genebridge4
RH8302 Stanford G3
GDB GDB:679049
G00-679-049

Mapping Information**View all results using the Map Viewer**

D10S2285	Sequence Map:	Chr 10	mv
	Position:	18102863-18103201 (bp)	
D10S2285	Sequence Map:	Chr 10	mv
	Position:	18349776-18350114 (bp)	
WI-7191	WI-YAC Map:	Chr 10	mv
	Position:	73 (ordinal)	
	Reference Interval:	WC10.1	
SHGC-12453	NCBI RH Map:	Chr 10	mv

Position: 240.4 (cR)
Lod score: 2.20

SHGC-12453 SHGC-G3 Map: Chr 10 mv
Position: 841 (cR10000)
Lod score: F
Reference Interval: 1000:1 bin 15

SHGC-12453 GM99-G3 Map: Chr 10 mv
Position: 841 (cR10000)
Lod score: F
Reference Interval: D10S1763-D10S548 (39.5-43.4 cM)

Electronic PCR results

RefSeq mRNA (1)

NM_002438.1 4617 .. 4955 Homo sapiens mannose receptor, C type 1 (MRC1) mRNA (5185 bp)

mRNA (2)

J05550.1 4617 .. 4955 Human mannose receptor mRNA, complete cds (5185 bp)
X55635.1 4590 .. 4928 H.sapiens mRNA for macrophage mannose receptor (5158 bp)

Genomic (2)

M93221.1 451 .. 789 Human macrophage mannose receptor (MRC1) gene, exon 30 (1206 bp)
AH002983.1 10082 .. 10420 Human macrophage mannose receptor (MRC1) gene (10837 bp)

Working Draft phase 1 (from GenBank HTGS division) (3)

AL157885.8 70884 .. 71222 Homo sapiens chromosome 9 clone RP11-530O10 map p24.1-24.3, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces (173117 bp)
AC011982.6 72104 .. 72442 Homo sapiens clone RP11-16N12, WORKING DRAFT SEQUENCE, 4 unordered pieces (168513 bp)
AC015944.3 59524 .. 59862 Homo sapiens chromosome 17 clone RP11-167J4 map 17, WORKING DRAFT SEQUENCE, 13 unordered pieces (137473 bp)

ESTs (5)

AL545341.1 343 .. 681 AL545341 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI027YH14 5 prime (908 bp)

AI458333.1	222 .. 560	tk07f04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2150335 3' similar to gb:J05550 MACROPHAGE MANNOSE RECEPTOR PRECURSOR (HUMAN); (714 bp)
AI539173.1	205 .. 543	tp78f04.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2205439 3' similar to gb:J05550 MACROPHAGE MANNOSE RECEPTOR PRECURSOR (HUMAN); (725 bp)
AI828628.1	200 .. 538	wc10f08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2314791 3' similar to gb:J05550 MACROPHAGE MANNOSE RECEPTOR PRECURSOR (HUMAN); (779 bp)
AW243257.1	221 .. 559	xn30b01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695177 3' similar to gb:J05550 MACROPHAGE MANNOSE RECEPTOR PRECURSOR (HUMAN); (724 bp)

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H. sapiens

M. musculus

R. norvegicus

D. rerio

D12S1936

UniSTS:7087

Primer Information

Forward primer:

ACAACTCAACATCCAGTTGGC

Reverse primer:

TTCATGTCTGTTTCAGCAGTATTG

PCR product size:

338-339 (bp), Homo sapiens

GenBank Accession:

G06674 J03746

Homo sapiens**Name:** D12S1936**Also known as:** G06674, J03746, WI-7728, RH8319, UTR-02230, SHGC-12779, G00-677-647**Cross References****LocusLink** LocusID:

4257

Symbol:

MGST1

Description:

microsomal glutathione S-transferase 1

Position:

12p12.3-p12.1

UniGene

Hs.389700

microsomal glutathione S-transferase 1

SNPrs1042669,
rs11875

Summary

RH details

RH8319

Genebridge4

RH8319

Stanford G3

GDB

GDB:677647

G00-677-647

Mapping Information**View all results using the Map Viewer**

D12S1936	Sequence Map:	Chr 12	mv
	Position:	16417253-16417591 (bp)	
SHGC-12779	GM99-G3 Map:	Chr 12	mv
	Position:	889 (cR10000)	
	Lod score:	F	
	Reference Interval:	D12S358-D12S1596 (27.2-48.1 cM)	

Electronic PCR results

mRNA (1)

J03746.1 552 .. 890 Human glutathione S-transferase mRNA,
complete cds (909 bp)

ESTs (5 of 6)[Show All Hits]

AA954788.1 18 .. 356 on56f08.s1 Soares_NFL_T_GBC_S1 Homo
sapiens cDNA clone IMAGE:1560711 3'
similar to gb:J03746 GLUTATHIONE
S-TRANSFERASE, MICROSOMAL
(HUMAN); (485 bp)

AA991209.1 23 .. 360 os24g11.s1 NCI_CGAP_Kid5 Homo
sapiens cDNA clone IMAGE:1606340 3'
similar to gb:J03746 GLUTATHIONE
S-TRANSFERASE, MICROSOMAL
(HUMAN); (489 bp)

AI080691.1 20 .. 359 oz35d12.x1 Soares_NhHMPu_S1 Homo
sapiens cDNA clone IMAGE:1677335 3'
similar to gb:J03746 GLUTATHIONE
S-TRANSFERASE, MICROSOMAL
(HUMAN); (462 bp)

AI281153.1 16 .. 354 qk58b12.x1 NCI_CGAP_Co8 Homo
sapiens cDNA clone IMAGE:1873151 3'
similar to gb:J03746 GLUTATHIONE
S-TRANSFERASE, MICROSOMAL
(HUMAN); (489 bp)

AI338121.1 19 .. 357 qt48d06.x1 Soares_fetal_Jung_NbHL19W
Homo sapiens cDNA clone
IMAGE:1951211 3' similar to gb:J03746
GLUTATHIONE S-TRANSFERASE,
MICROSOMAL (HUMAN); (489 bp)

Questions or Comments?

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UniSTS

Search for **SHGC-31620**

UniSTS:26485

Primer Information

Forward primer: CAGGATGAACCCAGGACG
Reverse primer: GGCAGAGTTGTCTATGTGCC
PCR product size: 209 (bp), Homo sapiens
GenBank Accession: G26619 G27088 M20681

Homo sapiens

Warning! This marker matched to multiple loci by e-PCR.

Name: SHGC-31620**Also known as:** G26619, G27088, M20681, SGC31620, RH14858, RH52614, STS_M20681**Cross References**

LocusLink LocusID: 6515
Symbol: SLC2A3
Description: solute carrier family 2 (facilitated glucose transporter), member 3
Position: 12p13.3

LocusLink LocusID: 144195
Symbol: SLC2A14
Description: solute carrier family 2 (facilitated glucose transporter), member 14
Position: 12p13.31

UniGene Hs.7594 solute carrier family 2 (facilitated glucose transporter), member 3
Hs.401274 solute carrier family 2 (facilitated glucose transporter), member 14

RH details RH14858 Genebridge4
RH14858 Stanford G3
RH52614 Genebridge4

Mapping Information**View all results using the Map Viewer**

SHGC-31620 Sequence Map:	Chr 12	mv
Position:	7866899-7867108 (bp)	
SHGC-31620 Sequence Map:	Chr 12	mv
Position:	7973997-7974205 (bp)	
SHGC-31620 NCBI RH Map:	Chr 12	mv

	Position:	151.1 (cR)	
	Lod score:	2.39	
SHGC-31620	SHGC-G3 Map:	Chr 12	mv
	Position:	515 (cR10000)	
	Lod score:	F	
	Reference Interval:	1000:1 bin 7	
SHGC-31620	TNG Map:	Chr 12	mv
	Lod score:	4.6	
	Reference Interval:	16	
SGC31620	WI-RH Map:	Chr 12	mv
	Position:	84.2 (cR3000)	
	Lod score:	P>3.00	
SHGC-31620	GM99-G3 Map:	Chr 12	mv
	Position:	515 (cR10000)	
	Lod score:	F	
	Reference Interval:	D12S99-D12S358 (13.9-27.2 cM)	
SGC31620	GM99-GB4 Map:	Chr 12	mv
	Position:	45.60 (cR3000)	
	Lod score:	3.00	
	Reference Interval:	D12S99-D12S358 (13.9-27.2 cM)	

Electronic PCR results

RefSeq mRNA (1)

NM_006931.1 1804 .. 2012 Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 3 (SLC2A3), mRNA (3915 bp)

mRNA (4)

M20681.1 1804 .. 2012 Human glucose transporter-like protein-III (GLUT3), complete cds (3915 bp)

AL832448.1 1515 .. 1723 Homo sapiens mRNA; cDNA DKFZp434F1129 (from clone DKFZp434F1129) (3270 bp)

AK074861.1 465 .. 673 Homo sapiens cDNA FLJ90380 fis, clone NT2RP2005027, highly similar to GLUCOSE TRANSPORTER TYPE 3, BRAIN (2568 bp)

BC039196.1 1699 .. 1907 Homo sapiens, solute carrier family 2 (facilitated glucose transporter), member 3, clone MGC:21198 IMAGE:4396508, mRNA, complete cds (3328 bp)

Genomic (2)

AH009611.1 13164 .. 13372 Homo sapiens glucose transporter 3 gene, complete cds (15346 bp)
AF274892.1 2497 .. 2705 Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds (4679 bp)

Low-pass Sequence Sampling (from GenBank HTGS division)
(1)

AC083975.1 17074 .. 17282 Homo sapiens chromosome 8 clone RP11-391E1 map 8, LOW-PASS SEQUENCE SAMPLING (61101 bp)

ESTs (5 of 8)[Show All Hits]

BF848098.1 40 .. 249 CM3-EN0047-031100-460-f07 EN0047 Homo sapiens cDNA (364 bp)
BG024237.1 145 .. 355 602302955F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4394676 5' (1177 bp)
BG114921.1 204 .. 423 602315141F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4415506 5' (1056 bp)
BG116331.1 179 .. 387 602318627F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4418694 5' (954 bp)
BG329890.1 257 .. 466 602429585F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4559325 5' (1102 bp)

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(18)



UniSTS

Search UniSTS for Go**D16S3225**

UniSTS:78497

Primer Information

Forward primer: **TTCCTCAGACGGAGGCTG**
Reverse primer: **GGAACATGGAGCTAGGTCTCC**
PCR product size: 109-110 (bp), Homo sapiens
GenBank Accession: G07192 X70218

Homo sapiens

Name: D16S3225
Also known as: G07192, X70218, WI-9235, RH82687, UTR-03753,
G00-678-185, SHGC-60989

Cross References

LocusLink LocusID: 5531
Symbol: PPP4C
Description: protein phosphatase 4 (formerly X), catalytic subunit
Position: 16p12-16p11
UniGene Hs.2903 protein phosphatase 4 (formerly X), catalytic subunit
RH details RH82687 Genebridge4
RH82687 Stanford TNG
GDB GDB:678185
G00-678-185

Mapping Information**View all results using the Map Viewer**

D16S3225 Sequence Map: Chr 16 mv
Position: 30094968-30095083 (bp)

Electronic PCR results**RefSeq mRNA (1)**

NM_002720.1 1091 .. 1206 Homo sapiens protein phosphatase 4 (formerly X), catalytic subunit (PPP4C) mRNA, and translated products (1429 bp)

mRNA (3)

BC001416.1	1131 .. 1246	Homo sapiens, protein phosphatase 4 (formerly X), catalytic subunit, clone MGC:1882, mRNA, complete cds (1369 bp)
AF097996.1	1091 .. 1206	Homo sapiens protein phosphatase X (PPX) mRNA, complete cds (1429 bp)
X70218.1	1122 .. 1231	Homo sapiens mRNA for protein phosphatase X (1360 bp)

Working Draft phase 1 (from GenBank HTGS division) (1)

AC138954.1	33111 .. 33226	Homo sapiens chromosome 16 clone RP11-828J20, WORKING DRAFT SEQUENCE, 5 unordered pieces (187383 bp)
------------	----------------	--

ESTs (5 of 78)[Show All Hits]

BF204450.1	116 .. 230	601866548F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4107107 5' (714 bp)
BF337359.1	249 .. 365	602035072F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183169 5' (574 bp)
BF512976.1	152 .. 268	UI-H-BW1-amh-b-07-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3069661 3' (333 bp)
BF593971.1	137 .. 253	THREONINE PROTEIN PHOSPHATASE 4 ; (558 bp)
N47803.1	137 .. 253	yy93f11.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:281133 3' similar to gb:X70218 PROTEIN PHOSPHATASE PP-X (HUMAN); (473 bp)

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(19)



UniSTS

Search UniSTS for Go

D19S1126

UniSTS:59528

Primer Information

Forward primer: GTTTAAAAAGTGACACCCATCTCC
Reverse primer: TGCCTCTGAAATGCCTCTTC
PCR product size: 134 (bp), Homo sapiens
GenBank Accession: G15092 T86191

Homo sapiens

Name: D19S1126
Also known as: , G15092, T86191, RH8874, SHGC-15376

Cross References

LocusLink LocusID: 3949
Symbol: LDLR
Description: low density lipoprotein receptor (familial hypercholesterolemia)
Position: 19p13.3
UniGene Hs.213289 low density lipoprotein receptor (familial hypercholesterolemia)
RH details RH8874 Genebridge4
RH8874 Stanford G3

Mapping Information**View all results using the Map Viewer**

D19S1126	Sequence Map:	Chr 19	mv
	Position:	11089504-11089637 (bp)	
SHGC-15376	SHGC-G3 Map:	Chr 19	mv
	Position:	25 (cR10000)	
	Lod score:	F	
	Reference Interval:	1000:1 bin 1	
SHGC-15376	GM99-G3 Map:	Chr 19	mv
	Position:	25 (cR10000)	
	Lod score:	F	
	Reference Interval:	pTEL-D19S413 (0-31.9 cM)	

Electronic PCR results

RefSeq mRNA (1)

NM_000527.2 4980 .. 5113 Homo sapiens low density lipoprotein receptor (familial hypercholesterolemia) (LDLR), mRNA (5175 bp)

Genomic (3)

L00352.1 2355 .. 2488 Human low density lipoprotein receptor gene, exon 18 (2550 bp)
AH002776.1 5956 .. 6089 Human low density lipoprotein receptor gene (6151 bp)
AF217403.1 33378 .. 33511 Homo sapiens low density lipoprotein receptor (LDLR) gene, partial cds (33567 bp)

ESTs (5 of 37)[Show All Hits]

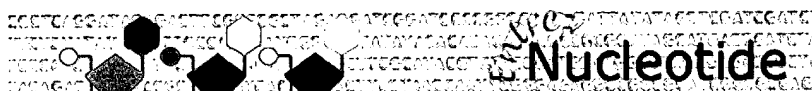
H68241.1 42 .. 175 yu69g03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:239092 3' similar to contains Alu repetitive element; (296 bp)
BF064095.1 68 .. 201 7h93h12.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3323591 3' (540 bp)
H91627.1 63 .. 196 yv03e11.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:241676 3' (316 bp)
H94628.1 43 .. 176 yw56g08.s1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:256286 3' (410 bp)
N39591.1 63 .. 196 yy51d05.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:277065 3' (470 bp)

Questions or Comments?

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(20)



Nucleotide

1: G11801. human STS WI-1027...[gi:1022556]

Links

LOCUS G11801 329 bp DNA linear STS 19-OCT-1995
DEFINITION human STS WI-10276, sequence tagged site.
ACCESSION G11801
VERSION G11801.1 GI:1022556
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 329)
AUTHORS Hudson,T.
TITLE Whitehead Institute/MIT Center for Genome Research; Physically
 Mapped ESTs
JOURNAL Unpublished (1995)
COMMENT

Contact: Thomas Hudson
 Whitehead Institute/MIT Center for Genome Research
 Whitehead Institute for Biomedical Research
 9 Cambridge Center, Cambridge MA 02142 USA
 Tel: 617 252 1900
 Fax: 617 252 1902
 Email: thudson@genome.wi.mit.edu

Primer A: TTATTGGTGGTGTCTGATGAGC
 Primer B: GGCTTCATCTCTCTTGGGG
 STS size: 282
 PCR Profile:

Presoak:
 Denaturation:
 Annealing: 56 degrees C
 Polymerization:
 PCR Cycles: 35
 Thermal Cycler:

Protocol:
 Template: 10 ng
 Primer: each 5 pM
 dNTPs: each 4 nM
 Taq Polymerase: 0.025 units/ul
 Total Vol: 20 ul

Buffer:
 MgCl2: 1.5 mM
 KCl: 50 mM
 Tris-HCL: 10 mM
 pH: 9.3

Prepared with primer pairs derived from dbEST accession T86696.

FEATURES
 source 1..329
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /map="(709-716)_A_1"
 STS 16..297

primer bind 16..37
primer bind complement(279..297)
BASE COUNT 62 a 84 c 107 g 72 t 4 others
ORIGIN

1 tttaangttt gatgtttatt ggtggtgtct gatgagcgtt tctcttgtcc agactgtgtt
61 tctctctcca gaccagctcc cagggtagag ggggtgggga gtaggtggtg gctgtgtcag
121 tgctggggcc tggngccact cctagggaa gagcaggtgg ggcctcgggg ggtctggccc
181 tagctctggc agatccatcc tcagtgaagc acatccctgg ggcaaaggca ctctgaggc
241 caagaccagc atgggcttga tggagccacc ccagggagcc ccaagagaga tgaagccatc
301 aataaagcgg nccttcaggg cctgggnct

//

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UniGene Cluster Hs.348401 *Homo sapiens***LCAT Lecithin-cholesterol acyltransferase**SEE ALSO: [LocusLink](#) | [OMIM](#) | [HomoloGene](#)**SELECTED MODEL ORGANISM PROTEIN SIMILARITIES**

organism, protein and percent identity and length of aligned region

<i>H.sapiens</i> :	sp:P04180 - LCAT_HUMAN Phosphatidylcholine-sterol acyltransferase precursor (Lecithin-cholesterol acyltransferase)	100 % / 440 aa (see ProtEST)
<i>M.musculus</i> :	sp:P16301 - LCAT_MOUSE PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (LECITHIN-CHOLESTEROL ACYLTRANSFERASE)	85 % / 440 aa (see ProtEST)
<i>R.norvegicus</i> :	pir:XXRTN - XXRTN phosphatidylcholine-sterol O-acyltransferase (EC 2.3.1.43) precursor - rat	86 % / 440 aa (see ProtEST)
<i>A.thaliana</i> :	ref:NP_564286.1 - expressed protein [<i>Arabidopsis thaliana</i>]	34 % / 373 aa (see ProtEST)
<i>C.elegans</i> :	ref:NP_492033.1 - phosphatidylcholine-sterol acyltransferase [<i>Caenorhabditis elegans</i>]	40 % / 338 aa (see ProtEST)

MAPPING INFORMATION

Chromosome:	16
Genome View:	Chromosome 16
OMIM Gene Map:	16q22.1
UniSTS entries:	stSG1784
UniSTS entries:	GDB:180918
UniSTS entries:	GDB:181557
UniSTS entries:	SHGC-61154
UniSTS entries:	WI-10276
Genomic Context:	Map View
Genomic Context:	Map View

EXPRESSION INFORMATION

Note: Highly represented (5.0 pct) in library [6397 FN0181](#)

cDNA sources: Liver and Spleen ;well-differentiated endometrial adenocarcinoma, 7 pooled tumors ;2 pooled high-grade transitional cell tumors ;head_neck ;ovary ;colon_normal ;total brain ;poorly differentiated adenocarcinoma with signet ring cell features ;Pooled human melanocyte, fetal heart, and pregnant uterus ;prostate_normal ;tumor, 5 pooled (see description) ;whole brain ;pooled ;meningioma ;Liver ;glioblastoma (pooled) ;breast ;heart ;lung ;anaplastic oligodendroglioma ;placenta ;testis_normal ;brain

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UniSTS

Search UniSTS ☐ for Go**D16S3224**

UniSTS:372

Primer Information

Forward primer: **AAAACTGAGGCCCTTGGG**
Reverse primer: **ATGCCTTGGGCAGTTACAAC**
PCR product size: **100-101 (bp), Homo sapiens**
GenBank Accession: **G07084 X52425**

Homo sapiens

Name: **D16S3224**
Also known as: **, G07084, X52425, WI-9023, UTR-00709, G00-678-075**

Cross References

LocusLink	LocusID:	3566
	Symbol:	IL4R
	Description:	interleukin 4 receptor
	Position:	16p11.2-12.1
UniGene	Hs.75545	interleukin 4 receptor
SNP	rs3024682, rs3024683	Summary
GDB	GDB:678Q75	
	G00-678-075	

Mapping Information**View all results using the Map Viewer**

D16S3224 Sequence Map: Chr 16 mv
Position: 27302673-27302773 (bp)

Electronic PCR results**RefSeq mRNA (1)**

NM_000418.1 2917 .. 3017 Homo sapiens interleukin 4 receptor (IL4R) mRNA (3597 bp)

mRNA (1)

X52425.1 2917 .. 3017 Human IL-4-R mRNA for the interleukin 4 receptor (3597 bp)

Genomic (1)

AF421855.1 24974 .. 25074 Homo sapiens interleukin 4 receptor
(IL4R) gene, complete cds (26550 bp)

ESTs (5 of 8)[Show All Hits]

BF663631.1	262 .. 362	602145332F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4309111 5' (960 bp)
BF663754.1	263 .. 363	602145480F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4309122 5' (921 bp)
BF976609.1	263 .. 363	602244292F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4335407 5' (796 bp)
AL578357.1	490 .. 590	AL578357 LT1_NFL006_PL2 Homo sapiens cDNA clone CS0DK010YI12 3 prime (926 bp)
BG286353.1	188 .. 288	602383124F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4500724 5' (761 bp)

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UniSTS

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Search UniSTS for Go

D2S2645

UniSTS:27965

Primer Information

Forward primer: CATCTCTCCAACCTCAACTCAACC
Reverse primer: TTTAGGGTTCCAAAGACTGGG
PCR product size: 99-100 (bp), Homo sapiens
GenBank Accession: G07172 M27190

Homo sapiens

Name: D2S2645
Also known as: , G07172, M27190, WI-9197, UTR-05810,
G00-678-164

Cross References

LocusLink LocusID: 5967
Symbol: REG1A
Description: regenerating islet-derived 1 alpha
(pancreatic stone protein, pancreatic
thread protein)
Position: 2p12
UniGene Hs.49407 regenerating islet-derived 1 alpha
(pancreatic stone protein, pancreatic
thread protein)
SNP rs12072, rs1522864 Summary
GDB GDB:678164
G00-678-164

Mapping Information**View all results using the Map Viewer**

D2S2645	Sequence Map:	Chr 2	mv
	Position:	79308118-79308217 (bp)	
WI-9197	WI-YAC Map:	Chr 2	mv
	Position:	318 (ordinal)	
	Reference Interval:	WC2.5	

Electronic PCR results**RefSeq mRNA (1)**

NM_002909.2	631 .. 730	Homo sapiens regenerating islet-derived 1 alpha (pancreatic stone protein, pancreatic thread protein) (REG1A), mRNA (784 bp)
mRNA (2)		
BC005350.1	631 .. 730	Homo sapiens, Similar to regenerating islet-derived 1 alpha (pancreatic stone protein, pancreatic thread protein), clone MGC:12447, mRNA, complete cds (784 bp)
M27190.1	652 .. 751	Homo sapiens secretory pancreatic stone protein (PSP-S) mRNA, complete cds (777 bp)
Genomic (1)		
J05412.1	3992 .. 4091	Human regenerating protein (reg) gene, complete cds (4251 bp)
Working Draft phase 1 (from GenBank HTGS division) (1)		
AC011993.6	203014 .. 203113	Homo sapiens chromosome 2 clone RP11-5F23, WORKING DRAFT SEQUENCE, 24 unordered pieces (208419 bp)
ESTs (5 of 96)[Show All Hits]		
BF196051.1	26 .. 125	hr81d07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134893 3' similar to SW:LITA_HUMAN P05451 LITHOSTATHINE 1 ALPHA PRECURSOR ; (622 bp)
W38384.1	29 .. 128	zc77b11.s1 Pancreatic Islet Homo sapiens cDNA clone IMAGE:328317 3' similar to gb:M18963 LITHOSTATHINE PRECURSOR (HUMAN); (413 bp)
W45438.1	34 .. 133	zc83d01.s1 Pancreatic Islet Homo sapiens cDNA clone IMAGE:328897 3' similar to gb:M18963 LITHOSTATHINE PRECURSOR (HUMAN); (430 bp)
BI324991.1	29 .. 128	ic20h03.x2 HR85 islet Homo sapiens cDNA 3' similar to SW:LITA_HUMAN P05451 LITHOSTATHINE 1 ALPHA PRECURSOR ; (430 bp)
BI325035.1	31 .. 130	ic21d10.x2 HR85 islet Homo sapiens cDNA 3' similar to SW:LITA_HUMAN P05451 LITHOSTATHINE 1 ALPHA PRECURSOR ; (398 bp)



UniSTS

Search UniSTS Go**D9S1707**

UniSTS:78937

Primer Information

Forward primer: **TTCTGAAAATATAACCAGCCATTG**
Reverse primer: **ACCATTTTCACATTATTTTGAAAGC**
PCR product size: 177-178 (bp), Homo sapiens
GenBank Accession: G05863 X77584

Homo sapiens

Name: D9S1707
Also , G05863, X77584, WI-7848, WIAF-578, RH14082,
known as: RH62682, UTR-04669, SHGC-12856

Cross References

LocusLink	LocusID:	7295
	Symbol:	TXN
	Description:	thioredoxin
	Position:	9q31
UniGene	Hs.432922	thioredoxin
SNP	rs2776, rs3190473, rs5843	Summary
RH details	RH14082	Genebridge4
	RH14082	Stanford G3
	RH62682	Genebridge4
GDB	GDB:588444	

Mapping Information

View all results using the Map Viewer

D9S1707	Sequence Map:	Chr 9	mv
	Position:	106463707-106463883 (bp)	
WI-7848	WI-RH Map:	Chr 9	mv
	Position:	413.0 (cR3000)	
	Lod score:	F	
WI-7848	WI-YAC Map:	Chr 9	mv
	Position:	309 (ordinal)	
	Reference Interval:	WC9.5	
SHGC-12856	GM99-G3 Map:	Chr 9	mv
	Position:	3608 (cR10000)	
	Lod score:	F	

Reference Interval: D9S176-D9S279 (104.9-120.4 cM)

WIAF-578 GM99-GB4 Map: Chr 9 mv
Position: 350.70 (cR3000)
Lod score: 0.00
Reference Interval: D9S176-D9S279 (104.9-120.4 cM)

Electronic PCR results

mRNA (1)

X77584.1 405 .. 582 thioredoxin (583 bp)

Genomic (2)

X70288.1 953 .. 1129 H.sapiens gene for thioredoxin, exons 4 and 5 (1394 bp)

X54541.1 990 .. 1166 H.sapiens Trx gene for thioredoxin, exon 4 and exon 5 (1404 bp)

ESTs (5 of 6)[Show All Hits]

BG210571.1 148 .. 324 RST30196 Athersys RAGE Library Homo sapiens cDNA (342 bp)

BG214878.1 137 .. 313 RST34533 Athersys RAGE Library Homo sapiens cDNA (336 bp)

BG219578.1 138 .. 314 RST39338 Athersys RAGE Library Homo sapiens cDNA (332 bp)

AI050078.1 17 .. 193 an35c03.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700644 3' similar to gb:X77584 THIOREDOXIN (HUMAN);contains element MER7 repetitive element ; (401 bp)

AI653621.1 18 .. 194 tz21b11.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2289213 3' similar to gb:X77584 THIOREDOXIN (HUMAN); (598 bp)

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UniSTS

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for

Go

SHGC-11498

UniSTS:42735

Primer Information

Forward primer: **GAATTAAATGAGGGCTGAAACG**
Reverse primer: **CATGTGCATATTTTCATTCCCC**
PCR product size: 131 (bp), Homo sapiens
GenBank Accession: G14572 T52830

Homo sapiens

Name: SHGC-11498
Also known as: G14572, T52830, RH13879, D2S2836, gdb:733324, gdb:735490

Cross References

LocusLink LocusID: 3488
Symbol: IGFBP5
Description: insulin-like growth factor binding protein 5
Position: 2q33-q36
UniGene Hs.380833 insulin-like growth factor binding protein 5
RH details RH13879 Genebridge4
RH13879 Stanford G3
GDB D2S2836
gdb:733324
gdb:735490

Mapping Information**View all results using the Map Viewer**

SHGC-11498 Sequence Map: Chr 2 mv
Position: 217504614-217504744 (bp)

SHGC-11498 NCBI RH Map: Chr 2 mv
Position: 1652.7 (cR)
Lod score: 1.62

SHGC-11498 SHGC-G3 Map: Chr 2 mv
Position: 8508 (cR10000)
Lod score: F
Reference Interval: 1000:1 bin 116

SHGC-11498 GM99-G3 Map: Chr 2 mv
Position: 9347 (cR10000)

Lod score: F

Reference Interval: D2S164-D2S163 (222.0-225.6 cM)

Electronic PCR results**mRNA (2)**

L27560.1 2 .. 132 Human insulin-like growth factor binding protein 5 (IGFBP5) mRNA (3672 bp)
AF147308.1 124 .. 254 Homo sapiens full length insert cDNA clone YA81B05 (374 bp)

Genomic (2)

L27559.1 1124 .. 1254 Human insulin-like growth factor binding protein 5 (IGFBP5) gene, partial exon 4 (1303 bp)
AH003147.1 3565 .. 3695 Human insulin-like growth factor binding protein 5 (IGFBP5) gene (3744 bp)

ESTs (5 of 18)[Show All Hits]

AV746775.1 158 .. 288 AV746775 NPC Homo sapiens cDNA clone NPCBJE02 5' (389 bp)
AU140606.1 518 .. 649 AU140606 PLACE3 Homo sapiens cDNA clone PLACE3000376 5' (776 bp)
AU140627.1 442 .. 572 AU140627 PLACE3 Homo sapiens cDNA clone PLACE3000412 5' (776 bp)
AU140641.1 67 .. 197 AU140641 PLACE3 Homo sapiens cDNA clone PLACE3000434 5' (812 bp)
BF923964.1 63 .. 193 MR2-NT0138-301100-004-g07 NT0138 Homo sapiens cDNA (521 bp)

Questions or Comments?
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UniSTS

Search UniSTS for Go**D2S2647**

UniSTS:57707

Primer Information

Forward primer: GTGACACCAGAATAATGAGTCTGC
Reverse primer: AACCCATTCTCTCATGACACG
PCR product size: 105-106 (bp), Homo sapiens
GenBank Accession: G07206 S62539

Homo sapiens

Name: D2S2647
Also , G07206, S62539, WI-9260, RH56733, RH77087,
known as: UTR-04169, G00-678-201, SHGC-55897

Cross References

LocusLink	LocusID:	3667
	Symbol:	IRS1
	Description:	insulin receptor substrate 1
	Position:	2q36
UniGene	Hs.96063	insulin receptor substrate 1
RH details	RH56733	Genebridge4
	RH77087	Genebridge4
	RH77087	Stanford TNG
GDB	GDB:678201	
	G00-678-201	

Mapping Information**View all results using the Map Viewer**

D2S2647	Sequence Map:	Chr 2	mv
	Position:	227564666-227564771 (bp)	
WI-9260	WI-YAC Map:	Chr 2	mv
	Position:	904 (ordinal)	
	Reference Interval:	WC2.16	
WI-9260	WI-RH Map:	Chr 2	mv
	Position:	1049.1 (cR3000)	
	Lod score:	P1.56	
WI-9260	GM99-GB4 Map:	Chr 2	mv
	Position:	702.62 (cR3000)	
	Lod score:	0.62	

Reference Interval: D2S351-D2S2158 (233.1-236.2 cM)

Electronic PCR results

RefSeq mRNA (1)

NM_005544.1 4985 .. 5090 Homo sapiens insulin receptor substrate 1 (IRS1) mRNA (5828 bp)

mRNA (1)

S62539.1 4985 .. 5090 insulin receptor substrate-1 [human, skeletal muscle, mRNA, 5828 nt] (5828 bp)

ESTs (5 of 21)[Show All Hits]

BF983959.1	252 .. 357	602304547F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4396210 5' (1070 bp)
BG181890.1	215 .. 320	RST744 Athersys RAGE Library Homo sapiens cDNA (391 bp)
BG181891.1	218 .. 323	RST745 Athersys RAGE Library Homo sapiens cDNA (765 bp)
BG188140.1	216 .. 321	RST7149 Athersys RAGE Library Homo sapiens cDNA (792 bp)
BG190813.1	215 .. 320	RST9888 Athersys RAGE Library Homo sapiens cDNA (815 bp)

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UniSTS

Search UniSTS for Go

D2S2633

UniSTS:16134

Primer Information

Forward primer: **AGTCATGGCAGCACCTGAG**
Reverse primer: **ACCACAGCAGCCTCCTTG**
PCR product size: 113-114 (bp), Homo sapiens
GenBank Accession: G07054 X53279

Homo sapiens

Name: D2S2633
Also known as: , G07054, X53279, WI-8964, RH57064, UTR-00084,
G00-678-049

Cross References

LocusLink LocusID: 251
Symbol: ALPPL2
Description: alkaline phosphatase, placental-like 2
Position: 2q37
UniGene Hs.333509 alkaline phosphatase, placental-like 2
RH details RH57064 Genebridge4
GDB GDB:678049
G00-678-049

Mapping Information**View all results using the Map Viewer**

D2S2633	Sequence Map:	Chr 2	mv
	Position:	233238979-233239092 (bp)	
WI-8964	WI-YAC Map:	Chr 2	mv
	Position:	929 (ordinal)	
	Reference Interval:	WC2.16	
WI-8964	WI-RH Map:	Chr 2	mv
	Position:	1066.7 (cR3000)	
	Lod score:	P0.08	
WI-8964	GM99-GB4 Map:	Chr 2	mv
	Position:	725.37 (cR3000)	
	Lod score:	0.00	
	Reference Interval:	D2S2158-D2S125 (236.2-269.5 cM)	

Electronic PCR results**RefSeq mRNA (1)**

NM_031313.1 2031 .. 2144 Homo sapiens alkaline phosphatase, placental-like 2 (ALPPL2), mRNA (2485 bp)

mRNA (5)

BC014139.1 2024 .. 2137 Homo sapiens, clone MGC:20678 IMAGE:4652865, mRNA, complete cds (2500 bp)

J04948.1 2028 .. 2141 Human alkaline phosphatase (ALP-1) mRNA, complete cds (2487 bp)

X53279.1 1980 .. 2093 Human mRNA for placental-like alkaline phosphatase (EC 3.1.3.1) (2480 bp)

X55958.1 2009 .. 2122 H.sapiens mRNA for alkaline phosphatase (2463 bp)

AB012642.1 757 .. 870 Homo sapiens mRNA for alkaline phosphatase, partial cds (1234 bp)

Genomic (1)

J03252.1 3798 .. 3911 Human alkaline phosphatase (ALPP) gene, complete cds (4556 bp)

Working Draft phase 1 (from GenBank HTGS division) (1)

AC074188.3 17097 .. 17210 Homo sapiens chromosome 2 clone RP11-341G20, WORKING DRAFT SEQUENCE, 17 unordered pieces (179816 bp)

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UniSTS

(27)

Search UniSTS for Go

G29848

UniSTS:40531

Primer Information

Forward primer: **CTTGGTTGGCAGCATTC**
Reverse primer: **TGACTTAATACTTTGGTAAGCCTGG**
PCR product size: 207 (bp), Homo sapiens
GenBank Accession: G29848

Homo sapiens

Name: G29848
Also known as: SHGC-35517

Cross References

LocusLink LocusID: 5591
Symbol: PRKDC
Description: protein kinase, DNA-activated, catalytic polypeptide
Position: 8q11
UniGene Hs.155637 protein kinase, DNA-activated, catalytic polypeptide

Mapping Information**View all results using the Map Viewer**

G29848 Sequence Map: Chr 8 mv
Position: 48409655-48409861 (bp)

Electronic PCR results**mRNA (1)**

U34994.3 12402 .. 12608 Homo sapiens DNA dependent protein kinase catalytic subunit (PRKDC)
mRNA, complete cds; alternatively spliced (12783 bp)

ESTs (3)

BF577070.1 47 .. 252 602135541F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4290347 5' (865 bp)
BF815967.1 62 .. 268 MR2-CI0127-051200-009-d04 CI0127 Homo sapiens cDNA (426 bp)



UniSTS

Search UniSTS for Go

D8S1948

UniSTS:76568

Primer Information

Forward primer: TTACAAAACATACCCAGTGTGTTGG
Reverse primer: CTTTTTAGTGCTTGAGACTGTCTCC
PCR product size: 110-111 (bp), Homo sapiens
GenBank Accession: G07089 M15856

Homo sapiens

Name: D8S1948
Also known as: , G07089, M15856, WI-9031, UTR-02606,
G00-678-079

Cross References

LocusLink	LocusID:	4023
	Symbol:	LPL
	Description:	lipoprotein lipase
	Position:	8p22
UniGene	Hs.180878	lipoprotein lipase
SNP	rs1837843	Summary
GDB	GDB:678079	
	G00-678-079	

Mapping Information**View all results using the Map Viewer**

D8S1948	Sequence Map:	Chr 8	mv
	Position:	19632196-19632306 (bp)	
WI-9031	WI-YAC Map:	Chr 8	mv
	Position:	72 (ordinal)	
	Reference Interval:	WC8.1	

Electronic PCR results**RefSeq mRNA (1)**

NM_000237.1 1673 .. 1783 Homo sapiens lipoprotein lipase
(LPL) mRNA (3549 bp)

mRNA (4)

BC011353.1	1560 .. 1670	Homo sapiens, Similar to lipoprotein lipase, clone MGC:17090 IMAGE:4177781, mRNA, complete cds (2315 bp)
M15856.1	1673 .. 1783	Human lipoprotein lipase mRNA, complete cds (3549 bp)
AK092286.1	1645 .. 1755	Homo sapiens cDNA FLJ34967 fis, clone NTONG2004690, highly similar to LIPOPROTEIN LIPASE PRECURSOR (EC 3.1.1.34) (2385 bp)
X14390.1	1616 .. 1726	Human mRNA for lipoprotein lipase (EC 3.1.1.34) (1924 bp)

Working Draft phase 1 (from GenBank HTGS division) (2)

AC015465.4	29737 .. 29847	Homo sapiens chromosome 8 clone RP11-35A5 map 8, WORKING DRAFT SEQUENCE, 31 unordered pieces (213943 bp)
AC074252.2	126080 .. 126190	Homo sapiens chromosome 8 clone RP11-677P13, WORKING DRAFT SEQUENCE, 14 unordered pieces (167705 bp)

ESTs (5)

BF107081.1	189 .. 299	601823640F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043744 5' (844 bp)
AL601082.1	301 .. 411	DKFZp313K0239_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone DKFZp313K0239 5' (717 bp)
AA180182.1	292 .. 405	zp48h11.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:612741 5' similar to gb:M15856 LIPOPROTEIN LIPASE PRECURSOR (HUMAN); (430 bp)
BM311959.1	86 .. 196	ig64d03.y1 HR85 islet Homo sapiens cDNA 5' (340 bp)
AA443878.1	192 .. 302	zw92h08.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:784479 5' similar to gb:M15856 LIPOPROTEIN LIPASE PRECURSOR (HUMAN); contains Alu repetitive element; (527 bp)

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(29)



UniSTS

Search UniSTS for Go

SGC35388

UniSTS:47321

Primer Information

Forward primer: GCAGAAAGTTGGGACTGAGC
Reverse primer: TGAAACTGACACATAAACCAAACC
PCR product size: 203 (bp), Homo sapiens
GenBank Accession: G28599 U21108

Homo sapiens

Name: SGC35388
Also known as: G28599, U21108, RH62105, SHGC-35388

Cross References

LocusLink	LocusID:	1846
	Symbol:	DUSP4
	Description:	dual specificity phosphatase 4
	Position:	8p12-p11
UniGene	Hs.2359	dual specificity phosphatase 4
SNP	rs674354	Summary
RH details	RH62105	Genebridge4

Mapping Information

View all results using the Map Viewer

SGC35388	Sequence Map:	Chr 8	mv
	Position:	29014820-29015022 (bp)	
SGC35388	WI-RH Map:	Chr 8	mv
	Position:	117.1 (cR3000)	
	Lod score:	P1.16	
SGC35388	GM99-GB4 Map:	Chr 8	mv
	Position:	116.89 (cR3000)	
	Lod score:	3.00	
	Reference Interval:	D8S1820-D8S505 (54.2-60.0 cM)	

Electronic PCR results

RefSeq mRNA (2)

NM_001394.3 1648 .. 1850 Homo sapiens dual specificity phosphatase 4 (DUSP4), transcript variant 1, mRNA (2514 bp)

NM_057158.2 2537 .. 2739 Homo sapiens dual specificity phosphatase 4 (DUSP4), transcript variant 2, mRNA (3404 bp)

mRNA (5)

U48807.1 1369 .. 1571 Human MAP kinase phosphatase (MKP-2) mRNA, complete cds (2241 bp)

BC002671.1 1417 .. 1619 Homo sapiens, dual specificity phosphatase 4, clone MGC:3713, mRNA, complete cds (1849 bp)

BC014565.1 1649 .. 1851 Homo sapiens, Similar to dual specificity phosphatase 4, clone MGC:2119 IMAGE:3050199, mRNA, complete cds (2100 bp)

AL137704.1 2537 .. 2739 Homo sapiens mRNA; cDNA DKFZp434O1321 (from clone DKFZp434O1321); partial cds (2981 bp)

U21108.1 1495 .. 1697 Human dual specific protein phosphatase mRNA, complete cds (2234 bp)

Working Draft phase 1 (from GenBank HTGS division) (2)

AC055851.3 105844 .. 106046 Homo sapiens chromosome 11 clone RP11-799H21 map 11, WORKING DRAFT SEQUENCE, 5 unordered pieces (196649 bp)

AC020588.6 23697 .. 23899 Homo sapiens chromosome 8 clone RP11-115B10, WORKING DRAFT SEQUENCE, 10 unordered pieces (191365 bp)

Low-pass Sequence Sampling (from GenBank HTGS division) (1)

AC090140.2 23558 .. 23760 Homo sapiens chromosome 8 clone RP11-125F4 map 8, LOW-PASS SEQUENCE SAMPLING (72663 bp)

ESTs (5 of 7)[Show All Hits]

AL526259.1 158 .. 360 AL526259 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC016YE19 3 prime (696 bp)

AL526295.1 336 .. 538 AL526295 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC016YE19 5 prime (768 bp)

AL528247.1 161 .. 362 AL528247 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC023YC01 3 prime (957 bp)

BG683635.1 127 .. 329 602651133T1 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:4761873 3' (665 bp)

(30)



UniSTS

Search UniSTS for Go

D10S2139

UniSTS:31654

Primer Information

Forward primer: CCCCATGTGACTTTATCTGTAGC
Reverse primer: AGTCTTGAGACGTCGTACTCCG
PCR product size: 267-268 (bp), Homo sapiens
GenBank Accession: G11293 L07032

Homo sapiens

Name: D10S2139
Also , G11293, L07032, UTR-9690, RH2032, RH51459,
known as: SHGC-9690, STSG-9690, gdb:675557

Cross References

LocusLink	LocusID:	5588
	Symbol:	PRKCQ
	Description:	protein kinase C, theta
	Position:	10p15
UniGene	Hs.211593	protein kinase C, theta
SNP	rs2236380	Summary
RH details	RH2032	Genebridge4
	RH2032	Stanford G3
	RH51459	Genebridge4
GDB	GDB:674813	
	gdb:675557	

Mapping Information**View all results using the Map Viewer**

SHGC-9690	NCBI RH Map:	Chr 10	mv
	Position:	132 (cR)	
	Lod score:	3.40	
UTR-9690	WI-YAC Map:	Chr 10	mv
	Position:	23 (ordinal)	
	Reference Interval:	WC10.0	
SHGC-9690	SHGC-G3 Map:	Chr 10	mv
	Position:	240 (cR10000)	
	Lod score:	F	
	Reference Interval:	1000:1 bin 1	

UTR-9690	WI-RH Map:	Chr 10	mv
	Position:	61.3 (cR3000)	
	Lod score:	P1.35	
SHGC-9690	GM99-G3 Map:	Chr 10	mv
	Position:	240 (cR10000)	
	Lod score:	F	
	Reference Interval:	D10S1713-D10S189 (13.0-17.3 cM)	
UTR-9690	GM99-GB4 Map:	Chr 10	mv
	Position:	56.10 (cR3000)	
	Lod score:	0.00	
	Reference Interval:	D10S1713-D10S189 (13.0-17.3 cM)	

Electronic PCR results

RefSeq mRNA (1)

NM_006257.1 2275 .. 2542 Homo sapiens protein kinase C, theta (PRKCQ) mRNA (2705 bp)

mRNA (1)

L07032.1 2275 .. 2542 Human protein kinase C theta (PKC) mRNA, complete cds (2705 bp)

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UniSTS

Search UniSTS for Go

D10S2141

UniSTS:20873

Primer Information

Forward primer: **ATTCCTGAGTCTTCCAGAGCC**
Reverse primer: **ATGACATTGACAATTTTGTGTTG**
PCR product size: **97-98 (bp), Homo sapiens**
GenBank Accession: **G11313 G13262 M21188**

Homo sapiens

Name: **D10S2141**
Also , **G11313, G13262, M21188, RH2057, UTR-9770,**
known as: **STSG-9770, gdb:675580, G00-674-882, SHGC-9770**

Cross References

LocusLink	LocusID:	3416
	Symbol:	IDE
	Description:	insulin-degrading enzyme
	Position:	10q23-q25
UniGene	Hs.1508	insulin-degrading enzyme
RH details	RH2057	Genebridge4
	RH2057	Stanford G3
GDB	GDB:674882	
	gdb:675580	
	G00-674-882	

Mapping Information**View all results using the Map Viewer**

D10S2141	Sequence Map:	Chr 10	mv
	Position:	94345284-94345381 (bp)	
D10S2141	WI-YAC Map:	Chr 10	mv
	Position:	346 (ordinal)	
	Reference Interval:	WC10.7	

Electronic PCR results**RefSeq mRNA (1)**

NM_004969.1 3153 .. 3250 Homo sapiens insulin-degrading enzyme (IDE), mRNA (3279 bp)

mRNA (2)

- M21188.1 3153 .. 3250 Human insulin-degrading enzyme (IDE)
mRNA, complete cds (3337 bp)
- AK093287.1 1728 .. 1825 Homo sapiens cDNA FLJ35968 fis,
clone TESTI2013053, highly similar to
INSULIN-DEGRADING ENZYME
(EC 3.4.24.56) (1867 bp)

ESTs (5 of 17)[Show All Hits]

- AU124138.1 82 .. 179 AU124138 NT2RM2 Homo sapiens
cDNA clone NT2RM2001726 5' (842
bp)
- AU130876.1 527 .. 624 AU130876 NT2RP3 Homo sapiens
cDNA clone NT2RP3001594 5' (814
bp)
- BG181933.1 202 .. 299 RST792 Athersys RAGE Library Homo
sapiens cDNA (363 bp)
- BG190363.1 56 .. 153 RST9428 Athersys RAGE Library
Homo sapiens cDNA (198 bp)
- BG217353.1 271 .. 368 RST37060 Athersys RAGE Library
Homo sapiens cDNA (841 bp)

Questions or Comments?
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UniSTS

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D12S2022

UniSTS:65926

Primer Information

Forward primer: **TCCACATCTTCTCAGTGTTTTAGC**
Reverse primer: **TCACAGTGACCAGTTGGCAT**
PCR product size: 337-338 (bp), Homo sapiens
GenBank Accession: G06359 Y00698

Homo sapiens

Name: D12S2022
Also known as: G06359, Y00698, WI-7025, RH13900, UTR-00564,
SHGC-12338, G00-678-960

Cross References

LocusLink	LocusID:	5213
	Symbol:	PFKM
	Description:	phosphofructokinase, muscle
	Position:	12q13.3
UniGene	Hs.75160	phosphofructokinase, muscle
SNP	rs14683, rs1802781, rs3189641, rs8977	Summary
RH details	RH13900	Genebridge4
	RH13900	Stanford G3
GDB	GDB:678960 G00-678-960	

Mapping Information**View all results using the Map Viewer**

D12S2022	Sequence Map:	Chr 12	mv
	Position:	48256298-48256635 (bp)	
WI-7025	WI-YAC Map:	Chr 12	mv
	Position:	163 (ordinal)	
	Reference Interval:	WC12.1	
SHGC-12338	TNG Map:	Chr 12	mv
	Lod score:	14.5	
	Reference Interval:	53	

SHGC-12338 GM99-G3 Map: Chr 12 mv
Position: 1850 (cR10000)
Lod score: F
Reference Interval: D12S333-D12S325 (53.3-70.6 cM)

Electronic PCR results

RefSeq mRNA (1)

NM_000289.1 2422 .. 2759 Homo sapiens phosphofructokinase,
muscle (PFKM) mRNA (2759 bp)

mRNA (5 of 6)[Show All Hits]

BC000534.1 2427 .. 2764 Homo sapiens, phosphofructokinase,
muscle, clone MGC:8699, mRNA,
complete cds (2821 bp)
BC007798.1 2314 .. 2651 Homo sapiens, Similar to
phosphofructokinase, muscle, clone
IMAGE:4124137, mRNA, partial cds
(2670 bp)
BC012799.1 2427 .. 2764 Homo sapiens, Similar to
phosphofructokinase, muscle, clone
MGC:2270 IMAGE:2964710, mRNA,
complete cds (2821 bp)
BC013298.1 2427 ... 2764 Homo sapiens, Similar to
phosphofructokinase, muscle, clone
MGC:3934 IMAGE:2964710, mRNA,
complete cds (2821 bp)
BC021203.1 2449 .. 2786 Homo sapiens, clone MGC:13291
IMAGE:4100117, mRNA, complete cds
(2819 bp)

ESTs (5 of 19)[Show All Hits]

AU143861.1 9 .. 346 AU143861 HEMBA1 Homo sapiens
cDNA clone HEMBA1000220
' (549 bp)
AA088885.1 4 .. 343 zn54a04.s1 Stratagene muscle 937209
Homo sapiens cDNA clone
IMAGE:561966 3' similar to
gb:M26066
6-PHOSPHOFRUCTOKINASE,
MUSCLE TYPE (HUMAN); (431 bp)
AA088897.1 28 .. 365 zn54f02.s1 Stratagene muscle 937209
Homo sapiens cDNA clone
IMAGE:562011 ' similar to
gb:M26066
6-PHOSPHOFRUCTOKINASE,
MUSCLE TYPE (HUMAN); (430 bp)
BM310330.1 1 .. 338 ih11c05.x1 Human insulinoma Homo
sapiens cDNA ' similar to
TR:P78457 P78457
6-PHOSPHOFRUCTOKINASE ; (553
bp)



UniSTS

Search for **D12S2096**

UniSTS:31887

Primer Information

Forward primer: **CCCGTGTGTTTCCTTTTCCTA**
Reverse primer: **AGGCACTCAGCCAACCTGTG**
PCR product size: **152 (bp), Homo sapiens**
GenBank Accession: **G13455**

Homo sapiens

Name: **D12S2096**
Also known as: **, G13455, RH7834, SHGC-10801, gdb:740726, gdb:741868**

Cross References

LocusLink LocusID: **517**
Symbol: **ATP5G2**
Description: **ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2**
Position: **12q13.13**
UniGene Hs.89399 **ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2**
SNP rs1803178, rs1803179 **Summary**
RH details RH7834 **Genebridge4**
RH7834 **Stanford G3**
GDB gdb:740726
gdb:741868

Mapping Information**View all results using the Map Viewer**

D12S2096	Sequence Map:	Chr 12	mv
	Position:	53775649-53775800 (bp)	
SHGC-10801	GM99-G3 Map:	Chr 12	mv
	Position:	2163 (cR10000)	
	Lod score:	F	
	Reference Interval:	D12S325-D12S1691 (70.6-73.5 cM)	

Electronic PCR results**RefSeq mRNA (1)**

NM_005176.3 530 .. 681

Homo sapiens ATP synthase, H+
transporting, mitochondrial F0
complex, subunit c (subunit 9),
isoform 2 (ATP5G2), mRNA (746
bp)**Genomic (1)**

X69908.1 14800 .. 14951

H.sapiens gene for mitochondrial
ATP synthase c subunit (P2 form)
(15016 bp)**Working Draft phase 1 (from GenBank HTGS division) (2)**

AC068986.21 46795 .. 46946

Homo sapiens chromosome 12
clone RP11-625F12, WORKING
DRAFT SEQUENCE, 11
unordered pieces (185029 bp)

AC010892.4 108945 .. 109096

Homo sapiens chromosome 12
clone RP11-462C10, WORKING
DRAFT SEQUENCE, 19
unordered pieces (184000 bp)**Low-pass Sequence Sampling (from GenBank HTGS division)
(1)**

AC091693.1 26997 .. 27148

Homo sapiens chromosome 8 clone
RP11-462D9 map 8, LOW-PASS
SEQUENCE SAMPLING (59897
bp)**Questions or Comments?
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UniSTS

Search for

A001U02

UniSTS:56220

Primer Information

Forward primer: **GTACAGATCGGAAGAAAGT**
 Reverse primer: **CCTTCCCTTCTACCTAAC**
 PCR product size: 106 (bp), Homo sapiens
 GenBank Accession: G19646

Homo sapiens

Name: A001U02
 Also known as: G19646, RH10457

Cross References

UniGene Hs.130607 mevalonate kinase (mevalonic aciduria)
 RH details RH10457 Genebridge4

Mapping Information

View all results using the Map Viewer

A001U02	NCBI RH Map:	Chr 12	mv
	Position:	711.3 (cR)	
	Lod score:	1.15	
A001U02	GM99-GB4 Map:	Chr 12	mv
	Position:	427.06 (cR3000)	
	Lod score:	1.31	
	Reference Interval:	D12S78-D12S79 (113.3-126.1 cM)	

Electronic PCR results

ESTs (1)

T15910.1 56..161 IB2063 Infant brain, Bento Soares Homo sapiens
 cDNA 3'end similar to H. sapiens mevalonate
 kinase mRNA (272 bp)

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Unit 1